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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:52:21; Search time 170.72 Seconds (without alignments) 25.057 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-331-631A-1_COPY_186_248
355
1 KRDPQQREYEDCRRRCEQQE.....MMNPQRGGSGRYEEGEEEQS 63

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	0	5	4	w	N	_	No.	Result
73	73	73	73	73	73	73.5	73.5	74	74	75		75.5	77	77.5	77.5	77.5	78	79	79	79.5	84	86	92	101	112	114	120	124	Score	
20.6	0.	0.	0	0.	0.	20.7	0	0	0	1.	21.3	21.3	1.	1.	1.	21.8			2		23.7		5	8	_	.2	33.8	4	Match	Query
3190	573	568	562	540	407	582	185	1898	1038	1090	834	330	646	911	910	613	1671	919	411.	236	966	1655	810	605	637	588	566	509	Length	
2	N	N	N	2	2	N	ν	ب ـــا	N	N	2	N	N	N	N	N	N	N	2	2	2	N	2	2	2	فسا	2	2	DB	
T13828	A53234	T26243	T26242	S21825	T02258	B53234	S71512	A45973	T02634	A41696	T42702	T25169	D82493	B34721	A34721	S27770	S71628	A39248	T29475	T01662	S25365	T13998	T44430	S06398	S35221	FWCNAB	S22477	S08059	Ħ	
CREB-binding prote			hypothetical prote	vicilin-like stora	globulin1 - maize	vicilin-like stora	hypothetical prote	trichohyalin - hum	=	н		hypothetical prote	conserved hypothet		androgen receptor	hypothetical prote	sensory transducti			ulin-1 - ma	protein - y	-	protein PV100 [imp			alpha-globulin B p	vicilin precursor	alpha-globulin typ	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
68	68	68.5	68.5	69	69	69	69	69	69	70.5	70.5	71	71	71	71.5
19.2	19.2	19.3	19.3	19.4	19.4	19.4	19.4	19.4	19.4	19.9	19.9	20.0	20.0	20.0	20.1
1154	1069	758	679	1023	449	449	448	410	133	1344	447	625	162	139	669
Ν	N	N	N	N	N	N	N	2	N	2	N	N	N	N	Ν
S69206	T00377	S54522	B75262	S12519	A39692	A38080	S33926	JC5046	I51960	T42637	S52391	A34615	S49259	A26892	JC5662
regulator protein	KIAA0642 protein -	hypothetical prote	conserved hypothet	glutactin - fruit	Wilms' tumor prote	Wilms tumor suscep	Wilms' tumor prote	Wilms' tumor suppr	WT1 zinc-finger ho	hypothetical prote	centrosomin B - mo	profilaggrin – rat	albumin 4 - easter	Mopa box protein -	hepatoma-derived g

ALIGNMENTS

RESULT 2 \$22477 vicilin precursor - cacao C:Species: Theobroma cacao (cacao) C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999 C:Accession: \$22477; \$22478; \$18105; \$22050 R:McHenry, L.; Fritz, p.J. Plant Mol. Biol. 18, 1173-1176, 1992 A:Fitle: Comparison of the structure and nucleotide sequence of vicilin genes A:Reference number: \$22477; MUID:92288309 A:Reference number: \$22477 A:Molecule type: DNA A;Residues: 1-56 <mch> A;Cross-references: EMBL:X62625 A;Cross-references: EMBL:X62626 A;Cross-references: EMBL:X62626 A;Cross-references: EMBL:X62626 A;Cross-references: EMBL:X62626 C:Genetics: A;Introns: 211/1: 269/3; 296/3; 391/3; 502/1 C;Superfamily: glycinin</mch>	Ouery Match 34.9%; Score 124; DB 2; Length 509; Best Local Similarity 37.0%; Pred. No. 9.1e-06; Matches 34; Conservative 9; Mismatches 15; Indels 34; Gaps 34; Gonservative 9; Mismatches 15; Indels 34; Gaps 34; Conservative 9; Mismatches 15; Indels 15; Indels 16; Indels 16; Indels 16; Indels 16; Indels 16; Indels 16; Indels	RESULT 1 S08059 alpha-globulin type B precursor (tandem 1) - upland cotton (fragment) N;Alternate names: seed storage protein C;Species: Gossyplum hirsutum (upland cotton) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993 C;Accession: S08059 R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987 A;Title: Developmental biochemistry of cottonseed embryogenesis and germination. A;Reference number: S06398 A;Accession: S08059 A;Status: not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-509 <chl> C;Superfamily: glycinin</chl>
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A; Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PI:A; Experimental source: var. Coker 201
R; Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A; Title: Developmental biochemistry of cottonseed embryogenesis
A; Reference number: S06398
A; Accession: S06911
A; Status: not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-81 <CH2>
C; Comment: This is a seed storage protein
C; Keywords: 91ycoprotein; seed; storage protein
F; 1-25/Domain: signal sequence #status predicted <SIG>
F; 26-588/Product: alpha-globulin storage protein #status predictin status predictin status predictin status predictin predictin signal sequence #status predictin #status predictin predictin signal sequence #status predictin #status predictin predictin status predictin #status predict
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R:Chlan, C.A.: Pyle, J.B.: Legocki, A.B.: Dure III, L. Plant Mol. Biol. 7, 475-489, 1986
A:Title: Developmental biochemistry of cottonseed embryogenesis
                                                                                     C; Accession: S35221
R; Heck, G.R.; Chamberlain, A.K.;
                                                                                                                                                globulin Beg1 precursor - barley
C;Species: Hordeum vulgare (barley)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994
                           A; Title:
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A; Molecule type: mRNA
A; Residues: 1-588 <CHL>
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. Genet. 239, 209-218, 1993
Barley embryo globulin 1 gene, Bonce number: S35221; MUID:93287988
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C;Genetics:
A;Gene: Beg1
A;Map position: 4
C;Superfamily: glycinin
C;Keywords: glycoprotein
F;174-190/Product: globulin B
A; Accession: T44430
A; Status: preliminary; ti
A; Molecule type: mRNA
A; Residues: 1-810 < YAM>
A; Cross-references: EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s06398
alpha-globulin type A precursor - upland cotton
N;Alternate names: seed storage protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
C;Accession: S06398
C;Accession: S06398
                                                                                    R; Yamada, K.; Shimada, T.; Kondo, M.; Nish
J. Biol. Chem. 274, 2563-2570, 1999
A;Title: Multiple functional proteins are
A;Reference number: Z22767; MUID:99107919
                                                                                                                                                       protein PV100 [imported] - winter squash
C;Species: Cucurbita maxima (winter squash)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change
C;Accession: T44430
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F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predicted
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A; Residues: 1-605 <CHL>
C; Superfamily: glycinin
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A; Status: not compared with
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C;Genetics:
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A; Molecule type: mRNA
A; Residues: 1-637 <HEC>
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                                                                                                                                                                                                                                                                                                                                                                                                        3 DPQQREYEDCRRRCEQQEPRQQHQCQLRCREQ-QRQHGRGGDMM--
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                                                                                                                                                                                                                                                                                                                                                                        DPQRR-YQDCRQHCQQEERRLRPHCEQSCREQYEKQQQQQPDKQFKECQQRCQWQEQRPE 137
                                                                                                                                                                                                                                                                                                     RKQQCVKECREQYQEDPWKGERENKWREEEEEES
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                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 27. 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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EMBL: AB019195; NID: g3808061;
                                                      translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                      NPQRG-GSGRYEEGEEEQS
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                                                                                                                                            Hara-Nishimura,
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jan-2000 C;Accession: S25365; S48277; S45980; S25404; S25405; A30906; S44692 R;Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H. Yeast 8, 397-408, 1992 A;Title: Molecular analysis of yeast chromosome II between CMD1 and LYS2: the A;Reference number: S25364; MUID:92327848
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A;Accession: T13998
A;Status: -----
                                                                                                                                                                                 A;Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55615.1; A;Note: the nucleotide sequence was submitted to the EMBL Data R;Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I. submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X66247; NID:g3548; PIDN:CAA46973.1; PID:g3550 R;Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H. Yeast 10, 1363-1361, 1994 Past 10, 1363-1361, 1994 Past 10, 1363-1361, 1994 Past 10, 1363-1361, 1995 Past 10, 1363-1361, 1995 Past 10, 1363-1361, 1995 Past 10, 
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C;Species: Drosophila virilis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
C;Accession: T13998
       A; Molecule type: DNA
A; Residues: 1-966 <F
A; Cross-references:
                                                                                                                 A; Reference number: S45927
A; Accession: S45980
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A; Residues: 1-966 <M
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A; Residues: 1-1655 < NEW>
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                                         1-966 <FE2>
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       EMBL: 235981;
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       NID: g536449;
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Pred. No. 0.25;
6; Mismatches 1
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Pred. No. 0.031;
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PIDN:CAA85069.1; PID:g536450; MIPS:YBR112d
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   hypothetical protein
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R;Hilton, H.; Gaut, B.S.
Genetics 150, 863-872, 1998
A;Title: Speciation and domestication in maize
A;Reference number: Z14386; MUID:98429537
A;Accession: T01662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: unassigned tetratricopeptide repeat p C;Keywords: nucleus; transcription regulation F;224-257/Domain: tetratricopeptide repeat homology F;262-295/Domain: tetratricopeptide repeat homology F;296-329/Domain: tetratricopeptide repeat homology F;330-363/Domain: tetratricopeptide repeat homology F;365-398/Domain: tetratricopeptide repeat homology F;365-398/Domain: tetratricopeptide repeat homology
                                                                                                                                                                               C; Superfamily:
                                                                                                                                                                                                   A; Introns:
                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                   A;Residues: 1-236 <HIL>
A;Cross-references: EMBL:AF064222; NID:g3414836; PIDN:AAC31465.1; PID:g3414837
                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: T01662
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Zea mays (maize)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999
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Gene 73, 97-111, 1988
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A;Residues: 1-546,'K',548-966 <SCH>
A;Cross-references: EMBL:M17826; NID:g172725;
                                                                                                                                                                                                                                       A; Experimental source: subspecies
                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-546, 'K', 548-966 <TRU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Schultz, J.; Carlson, M.
Mol. Cell. Biol. 7, 3637-3645, 1987
A;Title: Molecular analysis of SSN6, a gene functionally related
A;Reference number: S25404; MUID:88065502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: SGD:CYC8; SSN6; CRT8
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                                                                           17; Conservative
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17; Conser*
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                                                                                               22.4%;
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                                                                           Score 79.5; D
Pred. No. 0.21
8; Mismatches
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Pred. No. 0.25;
5; Mismatches
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-RSGEGSSEDERERK 85
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T01D1.6

Caenorhabditis elegans

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A;Cross-references: GB:R20132
R;Kuiper, G.G.J.M.; Faber, P.W.; van Rooij, H.
J. Mol. Endocrinol. 2, R1-R4, 1989
A;Title: Structural organization of the human
A;Reference number: A60946; MUID:89322749
A;Accession: A60946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Cross-references: GB:M27423; GB:M27430; NID:g178904; PIDN:AAA51886.1; PID:g178906 R:Faber, P.W.; Kuiper, G.G.J.M.; van Rooij, H.C.J.; van der Korput, J.A.G.M.; Brinkmann Mol. Cell. Endocrinol. 61, 257-262, 1989 A:Title: The N-terminal domain of the human androgen receptor is encoded by one, large A:Reference number: A30328; MUID:89137730 A;Accession: A30328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 24-Nov-1999
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 24-Nov-1999
C;Accession: A39248; A30328; A40109; A60946; A34942; A27653; A40108; A40494; A32224; & R.Lubahn, D.B.; Brown, T.R.; Simental, J.A.; Higgs, H.N.; Migeon, C.J.; Wilson, E.M.; Proc. Natl. Acad. Sci. U.S.A. 86, 9534-9538, 1989
A;Title: Sequence of the intron/exon junctions of the coding region of the human andro A;Reference number: A39248; MUID:90083302
A;Accession: A39248
                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 559-624 <LU2>
                                                                                                                                                                                                                                                                                                                                                                            A; Title: Cloning of human androgen receptor complementary DNA A; Reference number: A40109; MUID:88178112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-77,79-165,'A',167-389,'L',391-464,473-538 <FAB>
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A; Residues: 1-919 < LUB>
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A; Introns: 25/3; 304/3
C; Superfamily: gliadin
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                                                                                                                                                                                                                                                                                                                                                 A; Accession: A40109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Lubahn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB:M20260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 androgen receptor - human
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A; Residues: 1-411 <BRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches 21
                                                    Lubahn,
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;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                     Residues:
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                                 Endocrinol.
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                                                 D.B.; Joseph,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       D.B.; Joseph,
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                      536-540;587-591;626-631;723-726;770-774;814-818;867-870 <KUI>
.B.; Joseph, D.R.; Sar, M.; Tan, J.; Higgs, H.N.; Larson, R.E.; French, Inol. 2, 1265-1275, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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  androgen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.3%; Score 79; DB 2; 30.0%; Pred. No. 0.38; tive 12; Mismatches 2
                                                                                                                                                                                                                                        P.W.; van Rooij, H.C.J.; van der Korput, J.A.G.M.;
receptor: complementary
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deoxyribonucleic
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A;Accession.....
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-77,79-211,'R',213-471,473-919 <TIL>
A;Cross-references: GB:M21748; GB:J04150; NID:g178871;
A;Cross-references: GB:M21748; GB:M21748; GB:M21748;
A;Cross-references: GB:M21748; GB:M21748;
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 538/2; 589/1; 628/1; 724/1; 772/2; 816/1; 868/3
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology C;Keywords: DNA binding; steroid binding; transcription regulation; zinc finger F;557-815/Domain: erbA transforming protein homology <ERBA>
F;559-579/Region: zinc finger
F;595-619/Region: zinc finger
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A; Residues: 468-564, 'K', 566-919 <TRA>
A; Residues: 468-564, 'K', 566-919 <TRA>
A; Cross-references: GB:M20260; NID:g178891; PIDN:AAA51774.1; PID:g178892
A; Note: the authors translated the codon AAG for residue 565 as Glu
A; Note: the Authors translated the codon AAG for residue 565 as Glu
A; Note: the Authors translated the codon AAG for residue 565 as Glu
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Proc. Natl. Acad. Sci. U.S.A. 85, 7211-7215, 1988
A;Title: Structural analysis of complementary DNA
A;Reference number: A40494; MUID:89017168
A;Accession: A40494
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Science 240, 324-326, 1988
A;Title: Molecular cloning of human and rat complementary
A;Reference number: A40108; MUID:88178111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-919 <LU3>
A;Cross-references: GB.M20132; NID:g178627; PIDN:AAA51729.1; PID:g178628; GB:J03180
A;Trapman, J.; Klaassen, P.; Kuiper, G.G.J.M.; van der Korput, J.A.G.M.; Faber, P.W.;
Biochem. Biophys. Res. Commun. 153, 241-248, 1988
A;Title: Cloning, structure and expression of a cDNA encoding the human androgen rece
     Вb
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A;Residues: 557-614,'H',616-624 <MOW>
A;Cross-references: PIDN:AAB28340.1; PID:g425580
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R;Tilley, W.D.; Marcelli, M.; Wilson, J.D.; McPhaul,
Proc. Natl. Acad. Sci. U.S.A. 86, 327-331, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A40715; MUID:94019395 A;Accession: A40715
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A; Residues: 557-628 < CHA>
A; Cross-references: GB: M18624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: not compared with
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A; Residues: 1-74,79-89,'H',90-472,'GGG',473-474,'E',476-644,'N',646-919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A40108
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                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                              Matches
     58
                                                                                          5 QQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQ
QQQQQQ--QQQQQQQQQQQQQQQETSPRQQQQQQGEDGSPQAHRRGPTGYLVLDEEQQ
                                                                                                                                                                                                   19;
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                22.3%;
32.8%;
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                                                                                                                                                                                                                                           Score 79; Pred. No.
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                0.78;
                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                              22;
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                                                                                                                                                                                                                                                                                        Length 919
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                                                                                                                                                                                              Indels
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C;Accession: S27770

R;Bescansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Collins, F.H. submitted to the EMBL Data Library, June 1992

A;Description: Distinct families of site-specific retroposons occu
В
                                       20
                                                                                      В
                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-613 <BES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein 1 - African malaria mosquito (fragment) C; Species: Anopheles gambiae (African malaria mosquito) C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_charc; Accession: $27770
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C;Keywords: phosphoprotein; signal transduction
F;1520-1629/Domain: response regulator homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-149,'E',151-219,'TRVLKLIQSTNNWIYWY',238-1671 <SCW>
A;Cross_references: EMBL:X96869; NID:g1237201; PIDN:CAA65612.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: strain AX2; substrain 214
R;Schuster, S.C.; Noegel, A.A.; Oehme, F.; Gerisch,
submitted to the EMBL Data Library, March 1996
A;Description: The hybrid histidine kinase Doka is F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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A;Accession: S71628
                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:M93690; NID:g159615; PID:g159616
                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S27770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: dokA
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A; Accession: S78068
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A; Residues: 1-1670 <SCH>
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C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: nucleic acid sequence not shown
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EMBO J. 15, 3880-3889, 1996
                                                                                                                                                                               Query Match
Best Local S
Matches 19
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Best Local :
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                                                                                    245 QQQQQQQQRNQQREWQQQQQQQQQHQQREQQQQQRVQQQNQQHQRQQQQQQQQQQQR----QQ 30C
301 QQQQEQQ 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 QEDPPSSQQEEPPLSQQQQEQEQEQEQEQEQEEQSKQKIEGKGGGGEEEECEGGGGGEGE 20
                                                                                                                                                                             Local Similarity 28.4 nes 19; Conservative
                                          56 EEGEEEQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 ---RYEEGEEEQ 62
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                                                                                                                                1 KRDPQQREYEDCRRRCEQQEPRQQH-----QCQLRCREQQRQHGRGGDMMNPQRGGSGRY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KRDPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQ----HGRGGDMMNPQRGGSG--- 53
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27.8%;
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                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                             Score 77.5; DB Pred. No. 0.78; 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #text_change 09-Sep-1997
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RESULT

Search completed: March Job time: 547 sec

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C:Species: Homo sapiens (man)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-Sep-1997
C:Accession: A34721
                                                                                                                                                                                F;548-806/Domain: erbA transforming protein homology <ERBA>
F;550-570/Region: zinc finger
F;586-610/Region: zinc finger
                                                                                                                                                                                                                                                                                                                                   A; Title: Specific region in hormone binding domain A; Reference number: A34721; MUID:90258935 A; Accession: B34721
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                                                                                                                                                                                                                                                   C;Superfamily: unassigned
C;Keywords: zinc finger
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A; Residues: 1-911 <GO2>
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R;Govindan, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Homo sapiens (man)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-Sep-1997
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C;Keywords: zinc finger
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C; Species:
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A; Residues: 1-910 <GOV>
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Best Local Similarity
Matches 19; Conserv
                                                                                Query Match
Best Local Similarity
Matches 19; Conserv
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58 QQQQQQ----QQQQQQQQQQQQQQQETSPRQQQQQQGEDGSPQAHRRGPTGYLVLDEEQQ 112
                                         5 QQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 QQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor A - human
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                                                                                                 21.8%; 32.8%;
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                                                                                14;
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                                                                              Score 77.5; D
Pred. No. 1.1;
14; Mismatches
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Pred. No. 1.1;
14; Mismatches
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